Gene name: O1-180

cDNA sequence: 1276 bp

"AAGGCGGGCGAGGCGCGGGACGCACCCATGTTCCCGGCGAG
CACGTTCCACCCCTGCCCGCATCCTTATCCGCAGGCCACCAAAGCCGGGGATG
GCTGGAGGTTCGGAGCCAGGGGCTGCCGACCCGCGCCCCCCTCCTTCCTCCCC
GGCTACAGACAGCTCATGGCCGCGGAGTACGTCGACAGCCACCAGCGGGCAC
AGCTCATGGCCCTGCTGTCGCGGATGGGTCCCCGGTCGGTCAGCAGCCGTGA
CGCTGCGGTGCAGGTGAACCCGCGCCGCGACGCCTCGGTGCAGTGTTCACTC
GGGCGCCGCACGCTGCAGCCTGCAGGGTGCCGAGCCAGCCCCGACGCCCGAT
CGGGTTCCTGTCAACCCCGTGGCCACGCCGGCGCCGGGAGATCCCCGCGATC
CTGGCAGACCGTAGCCCCGTTCTCGTCCGTGACCTTCTGTGGCCTCTCCTCCTC
ACTGGAGGTTGCGGGAGGCAGGCAGACACCCACGAAGGGAGAGGGGAGCCC
GGCATCCTCGGGGACCCGGGAACCGGAGCCGAGAGAGGTGGCCGCGAGGAA
AGCGGTCCCCCAGCCGCGAAGCGAGGAGGGCGATGTTCAGGCTGCAGGGCA
GGCCGGGTGGGAGCAGCAGCCACCACCGGAGGACCGGAACAGTGTGGCGGC
GATGCAGTCTGAGCCTGGGAGCGAGGAGCCATGTCCTGCCGCAGAGATGGCT
CAGGACCCCGGTGATTCGGATGCCCCTCGAGACCAGGCCTCCCCGCAAAGCAC
GGAGCAGGACAAGGAGCGCCTGCGTTTCCAGTTCTTAGAGCAGAAGTACGGCT
ACTATCACTGCAAGGACTGCAAAATCCGGTGGGAGAGCGCCTATGTGTGGTGT
GTGCAGGGCACCAGTAAGGTGTTACTTCAAACAGTTCTGCCGAGTGTGTGAGAA
ATCCTACAACCCTTACAGAGTGGAGGACATCACCTGTCAAAGTTGTAAAAGAAC
TAGATGTGCCTGCCCAGTCAGATTTCGCCACGTGGACCCTAAACGCCCCCATC
GGCAAGACTTGTGTGGGAGATGCAAGGACAAACGCCTGTCCTGCGACAGCAC
CTTCAGCTTCAAATACATCATTTAGTGAGAGTCGAAAACGTTTCTGCTAGATGG
GGCTAATGGAATGGACAAGTGAGCTTTCTCCCCTCTTCACCTCTTCCCTTTCCAA
ATTCTTCATGACAGACAGTGTTACTTGGATATAAAGCCTGTGAATAAAAGGTAT
TGCAAACAAAAAAAAAAAAAAAAAA"

Figure 1

Amino Acid sequence: 361aa

"MFPASTFHPCPHPYPQATKAGDGWRFGARGCRPAPPSFLPGYRQLMAAEYVDS
HQRAQLMALLSRMGPRSVSSRDAAVQVNPRRDASVQCSLGRRTLQPAGCRASPDA
RSGSCQPRGHAGAGRSPRSWQTVAPFSSVTFCGLSSSLEVAGGRQTPTKGEGSPA
SSGTREPEPREVAARKAVPQPRSEEGDVQAAGQAGWEQQPPPEDRNSVAAMQSEP
GSEEPCPAAEMAQDPGDSDAPRDQASPQSTEQDKERLRFQFLEQKYGYYHCKDCK
IRWESAYVWCVQGTSKVYFKQFCRVCEKSYNPYRVEDITCQSCKRTRCACPVRFR
HVDPKRPHRQDLCGRCKDKRLSCDSTFSFKYII"

Figure 2

O1-184 cDNA sequence: 1817bp

GTCACAGCTTTCCCCTGCCCGAATATGGTGATCTGTCTCCATTGTCCAGATCA
GGATGATTCTTTAGAAGAAGTCACAGAGGAATGCTATTCCCCACCCACCCTC
CAGAACCTGGCAATTCAGAGTCTACTGAGGGATGAGGCCTTGGCCATTTCTG
CTCTCACGGACCTGCCCCAGAGTCTGTTCCCAGTAATTTTTGAGGAGGCCTTC
ACTGATGGATATATAGGGATCTTGAAGGCCATGATACCTGTGTGGCCCTTCCC
ATACCTTTCTTTAGGAAAGCAGATAAATAATTGCAACCTGGAGACTTTGAAG
GCTATGCTTGAGGGACTAGATATACTGCTTGCACAAAAGGTTCAAACCAGTA
GGTGCAAACTCAGAGTAATTAATTGGAGAGAAGATGACTTGAAGATATGGGC
TGGATCCCATGAAGGTGAAGGCTTACCAGATTTCAGGACAGAGAAGCAGCCA
ATTGAGAACAGTGCTGGCTGTGAGGTGAAGAAAGAATTGAAGGTGACGACT
GAAGTCCTTCGCATGAAGGGCAGACTTGATGAATCTACCACATACTTGTTGC
AGTGGGCCCAGCAGAGAAAAGATTCTATTCATCTATTCTGTAGAAAGCTACT
AATTGAAGGCTTAACCAAAGCCTCAGTGATAGAAATCTTCAAAACTGTACAC
GCAGACTGTATACAGGAGCTTATCCTAAGATGTATCTGCATAGAAGAGTTGG
CTTTTCTTAATCCCTACCTGAAACTGATGAAAAGTCTTTTCACACTCACACTA
GATCACATCATAGGTACCTTCAGTTTGGGTGATTCTGAAAAGCTTGATGAGG
AGACAATATTCAGCTTGATTTCTCAACTTCCCACACTCCACTGTCTCCAGAAA
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GTGCCTGAAAAAGCCCTTGGAGACACTTTGCATCAGTAACTGTGACCTCTCAC
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CTCCTTGAGAGAGTTGGAGATACCCTGAAAACCCTGGAATTGGATTCATGTT
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CACCTCAGAGAGGTCACTTTCTATGATAATGATGTTTCTCTGCCTTTCTTGAA
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CCTGCCCCTCTAGAGTGCTATGATGACAGTGGTGTAATACTAACACACAGATT
AGAAAGTTTTTGTCCTGAGCTTCTGGATATACTGAGAGCCAAAAGACAGCTC
CATAGTGTCTCCTTTCAAACAACCAAATGCTCTAAATGTGGTGGGTGCTACAT
TTATGATCGGCATACCCAATGTTGCCGTTTTGTGGAACTACTATAAGCTTGAT
TGTGAAACTGAGAAATAGAAACTTAGTATTGGGGACTGATGAAATCCTAAGT
GAATGTCCACTGCTAAATGGAGCATGAAAATGTCAATCACCTAAAAGTCTGA
GATACACAGGAAAGTCAATAACTTCCTCTGAGCTGGTGAATGGATGTTGCAT
CTGTAGAAAGTATCAAGCACTTGTAGTTTGAATGTGTTACAATAGAAGCACC
ATTTTATGAGACTGGCCCAATCTGTTGACTGCATACAATAAATCTGTTGACTT
ATTAAATTTTTAAAAAAAAAAAAAAAAAAAAA

Figure 3

O1-184 amino acid sequence: 426 amino acids

MVICLHCPDQDDSLEEVTEECYSPPTLQNLAIQSLLRDEALAISALTDLPQSLFP
VIFEEAFTDGYIGILKAMIPVWPFPYLSLGKQINNCNLETLKAMLEGLDILLAQKV
QTSRCKLRVINWREDDLKIWAGSHEGEGLPDFRTEKQPIENSAGCEVKKELKV
TTEVLRMKGRLDESTTYLLQWAQQRKDSIHLFCRKLLIEGLTKASVIEIFKTVHA
DCIQELILRCICIEELAFLNPYLKLMKSLFTLTLDHIIGTFSLGDSEKLDEETIFSLIS
QLPTLHCLQKLYVNDVPFIKGNLKEYLRCLKKPLETLCISNCDLSQSDLDCLPYC
LNICELKHLHISDIYLCDLLLEPLGFLLERVGDTLKTLELDSCCIVDFQFSALLPAL
SQCSHLREVTFYDNDVSLPFLKTTSTPHSPAESADL

Figure 4

Gene name: O1-236

cDNA sequence: 1019bp

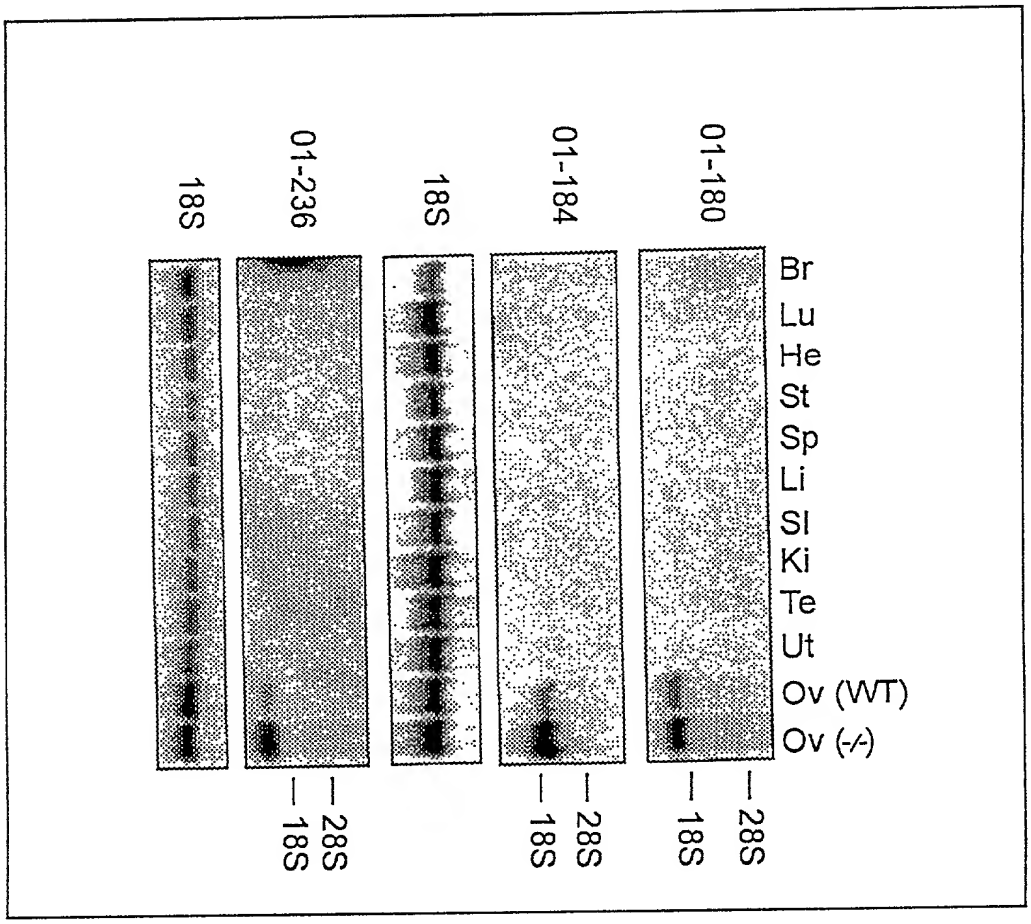
"GCCATATTGAGGACCTGCAGTAGAGGTGGAACCCATGACTGGCAGCGCAAAC
ACAGTGATAACAGCTGAGCTCCAAGCAAGGACCCAGGACCTTGCCTCACCACA
GACATAATCTTTCCCCACAACACCTCCACCAAGCCGCCCTGTAAATCGACATGA
GTCGCCACAGCACCAGCAGCGTGACCGAAACCACAGCAAAAAACATGCTCTGG
GGTAGTGAACTCAATCAGGAAAAGCAGACTTGCACCTTTAGAGGCCAAGGCGA
GAAGAAGGACAGCTGTAAACTCTTGCTCAGCACGATCTGCCTGGGGGAGAAAG
CCAAAGAGGAGGTGAACCGTGTGGAAGTCCTCTCCCAGGAAGGCAGAAAACC
ACCAATCACTATTGCTACGCTGAAGGCATCAGTCCTGCCCATGGTCACTGTGTC
AGGTATAGAGCTTTCTCCTCCAGTAACTTTTCGGCTCAGGACTGGCTCAGGACC
TGTGTTCCTCAGTGGCCTGGAATGTTATGAGACTTCGGACCTGACCTGGGAAG
ATGACGAGGAAGAGGAGGAAGAGGAGGAGGAAGAGGATGAAGATGAGGATG
CAGATATATCGCTAGAGGAGATACCTGTCAAACAAGTCAAAAGGGTGGCTCCC
CAGAAGCAGATGAGCATAGCAAAGAAAAAGAAGGTGGAAAAAGAAGAGGATG
AAACAGTAGTGAGGCCCAGCCCTCAGGACAAGAGTCCCTGGAAGAAGGAGAA
ATCTACACCCAGAGCAAAGAAGCCAGTGACCAAGAAATGACCTCATCTTAGCAT
CTTCTGCGTCCAAGGCAGGATGTCCAGCAGCTGTGTTTTGGTGCAGGTGTCCA
GCCCCACCACCCTAGTCTGAATGTAATAAGGTGGTGTGGCTGTAACCCTGTAAC
CCAGCCCTCCAGTTTCCGGAGGTTTTTGGTGAAGAGCCCCCAGCAAGTTCGCC
TAGGGCCACAATAAAATTTGCATGATCAGGAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA"

Figure 5

Amino Acid sequence: 207aa

" MSRHSTSSVTETTAKNMLWGSELNQEKQTCTFRGQGEKKDSCKLLLSTICLGEK
AKEEVNRVEVLSQEGRKPPITIATLKASVLPMVTVSGIELSPPVTFRLRTGSGPVFLS
GLECYETSDLTWEDDEEEEEEEEEEDEDEDADISLEEIPVKQVKRVAPQKQMSIAKK
KKVEKEEDETVVRPSPQDKSPWKKEKSTPRAKKPVTKK"

Figure 6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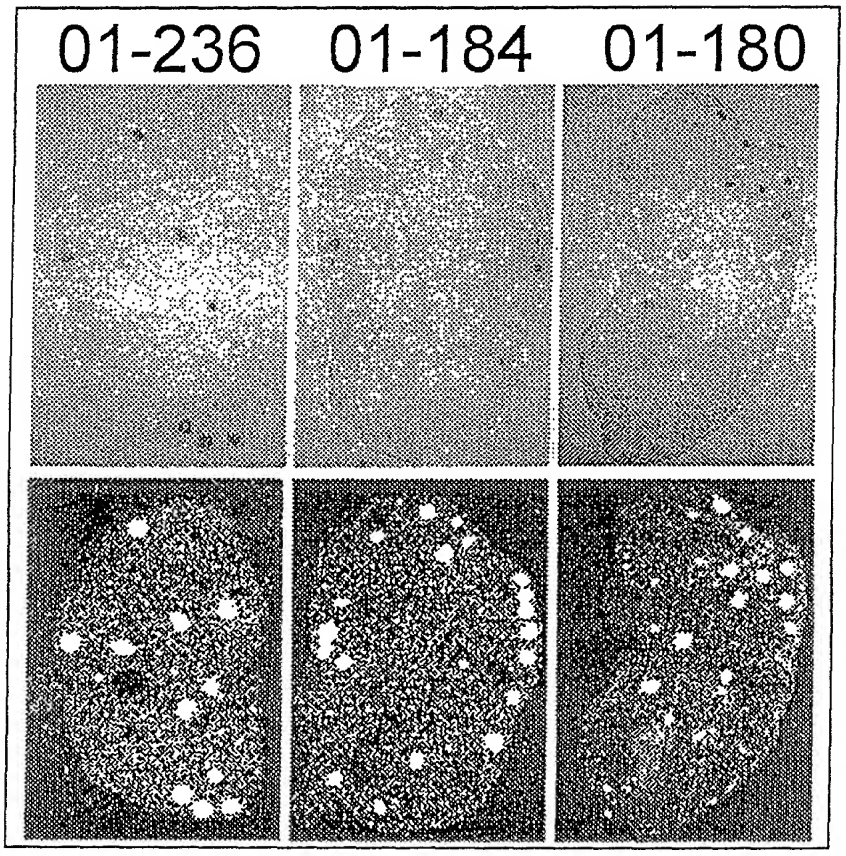
18S
Br
Lu
He
St
Sp
Li
Sl
Ki
Te
Ut
Ov (WT)
Ov (-/-)
28S
18S
28S
18S
28S
18S

Figure 7



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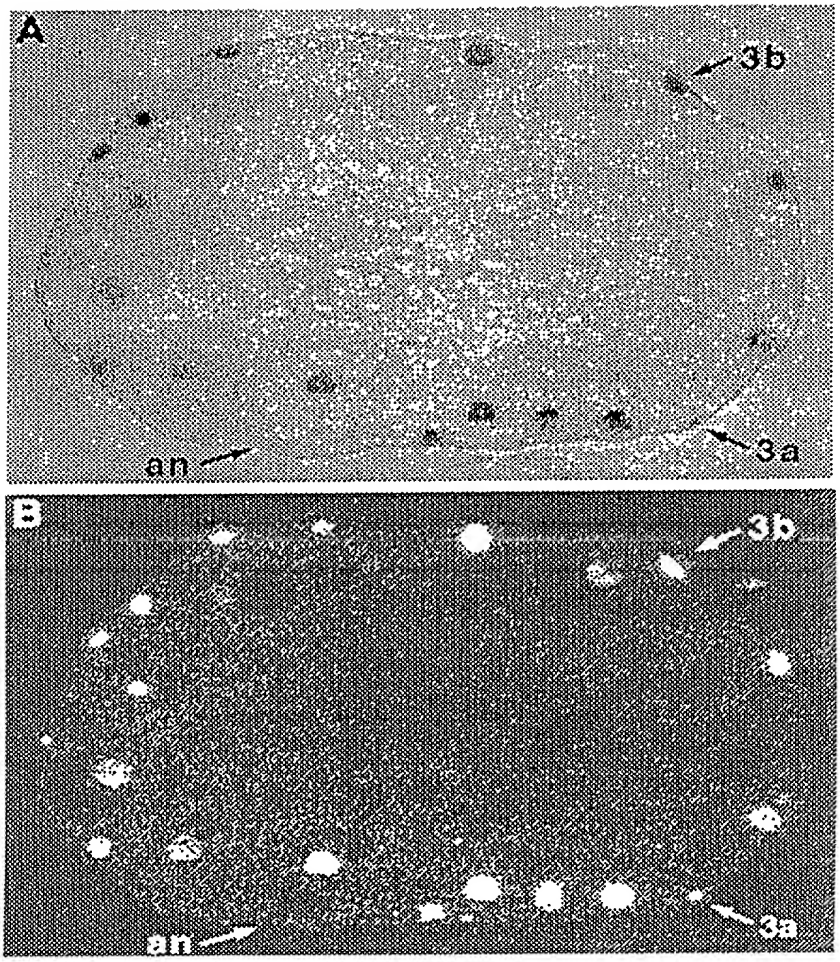


Figure 9

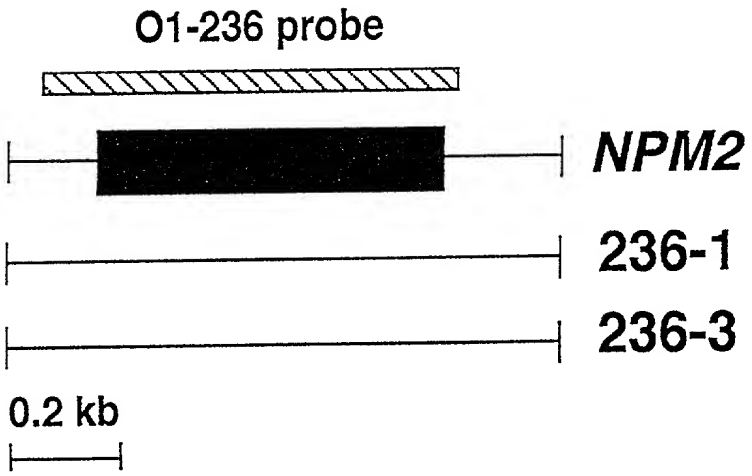
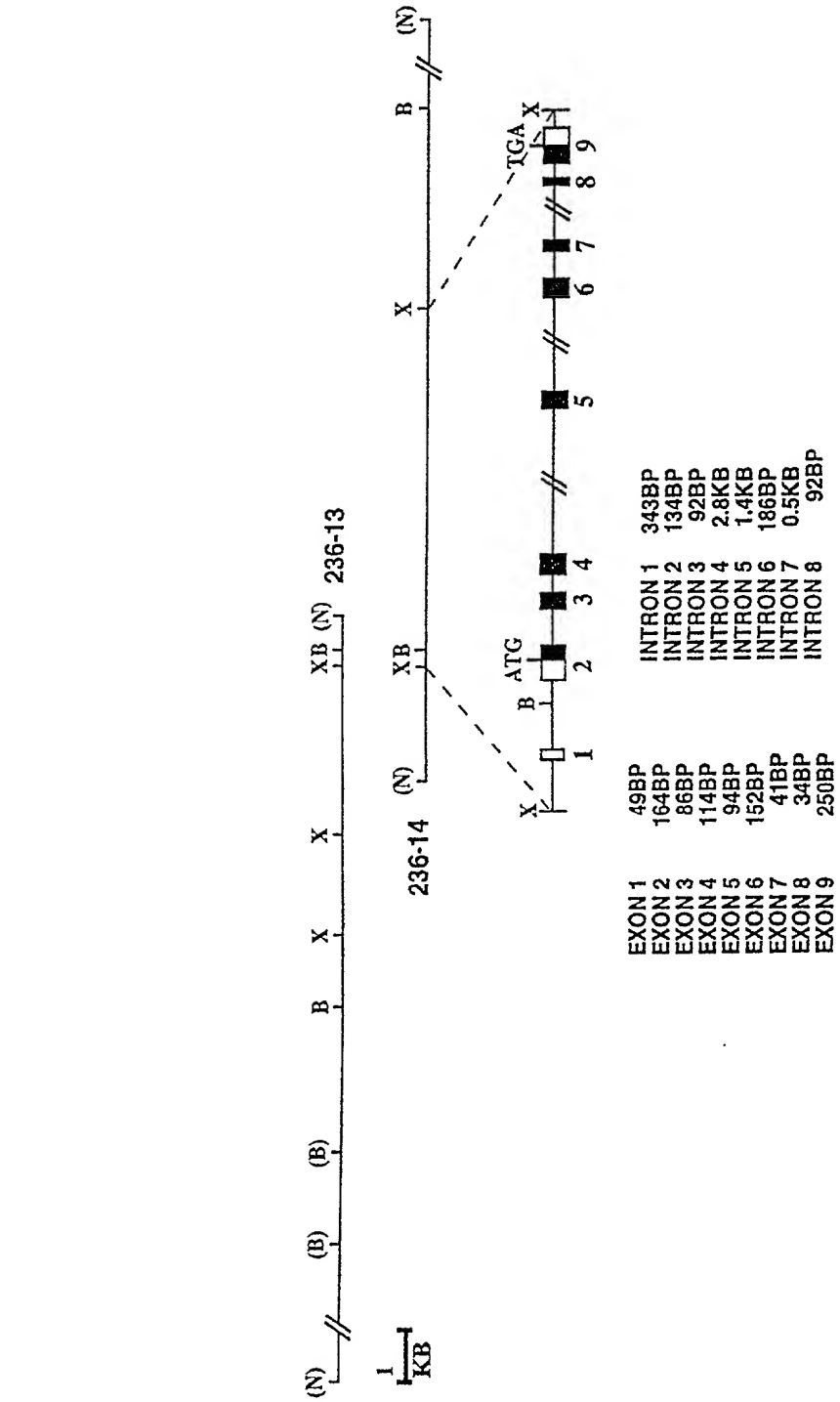


Figure 10


Npm2 MSRHSTSSVTETTAK--NMLWGSELN-QEKQTCTFRGQG-EKKDSCKLLL
Xnpm2 MA--STVSNTSKLEKPVSLIWGCELNEQDK-TFEFKVEDDEEKCEHQLAL
PKC
47 STICLGEKAKEEVNRVEVLSQE-GRKPPITIATLKASVLPMVTVSGIELS
48 RTVCLGDKAKDEFNIVEIVTQEEGAEKSVPIATLKPSILPMATMVGIELT
PKC
CK2
96 PPVTFRLRTGSGPVFLSGLECYETSDLTWEDDEEEEEEEEEEDEDEDADI
98 PPVTFRLKAGSGPLYISGQHVAMEEDYSWAEEEDEGEAEGEEEEEEEED-
CK2
146 SLEEIPVKQVKRVAPQKQMSIAKKKKVEKEEDETVVRPSPQDKSPWKKEK
147 --QESPPKAVKRPAATKKAGQAKKKKLDKE-DE------SSEEDSPTKKGK
196 STPRAKKPVTKK 207
189 GAGRGRKPAAKK 200

Figure 11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(B)
(B)
B
X
X
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1
KB
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B
ATG
TGA
X
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EXON 1 49BP
EXON 2 164BP
EXON 3 86BP
EXON 4 114BP
EXON 5 94BP
EXON 6 152BP
EXON 7 41BP
EXON 8 34BP
EXON 9 250BP
INTRON 1 343BP
INTRON 2 134BP
INTRON 3 92BP
INTRON 4 2.8KB
INTRON 5 1.4KB
INTRON 6 186BP
INTRON 7 0.5KB
INTRON 8 92BP

Figure 12

Mouse *Npm2* Gene Sequences

```
acagcagaggtgatgctcagaaatcaagttttaacagagggccaggtg
cttctagagtaggaggggattgcacacctccccacccccctcctctttc
ccaggcttcttaacagcctgctgtgggaagctgacccttagatggagc
cctgaaGCCATATTGAGGACCTGCAGTAGAGGTGGAACCCATGACTGG
CAGCGCAgtaagcttgagcagg... intron 1= 343bp
...ctttgcattactcagAACACAGTGATAACAGCTGAGCTCCAAGCA
AGGACCCAGGACCTTGCCTCACCACAGACATAATCTTTCCCCACAACA
CCTCCACCAAGCCGCCCTGTAAATCGAC    ATG AGT CGC CAC AGC
1                                                M   S   R   H   S

ACC AGC AGC GTG ACC GAA ACC ACA GCA AAA AAC ATG
6    T   S   S   V   T   E   T   T   A   K   N   M

CTC TGG Ggtaagggctaaggct... intron 2 = 134bp
18   L   W

...gtcttcgctgtgcagGT AGT GAA CTC AAT CAG GAA AAG
20                G   S   E   L   N   Q   E   K

CAG ACT TGC ACC TTT AGA GGC CAA TGC GAG AAG AAG
28   Q   T   C   T   F   R   G   Q   C   E   K   K

GAC AGC TGT AAA CTC TTG CTC AGC ACGgtgggtgtctccc
40   D   S   C   K   L   L   L   S   T

aa... intron 3 = 92bp  ...catcacctttctcagATC
49                                              I

TGC CTG GGG GAG AAA GCC AAA GAG GAG GTG AAC CGT
50   C   L   G   E   K   A   K   E   E   V   N   R

GTG GAA GTC CTC TCC CAG GAA GGC AGA AAA CCA CCA
62   V   E   V   L   S   Q   E   G   R   K   P   P

ATC ACT ATT GCT ACG CTG AAG GCA TCA GTC CTG CCC
74   I   T   I   A   T   L   K   A   S   V   L   P

ATGgtgagtcttctctcc... intron 4 = 2.8kb  ...agaa
86   M

gggggacacagGTC ACT GTG TCA GGT ATA GAG CTT TCT
87              V   T   V   S   G   I   E   L   S

CCT CCA GTA ACT TTT CGG CTC AGG ACT GGC TCA GGA
96   P   P   V   T   F   R   L   R   T   G   S   G
```

Figure 13A

```
        CCT GTG TTC CTC AGT GGC CTG GAA TGT TAT Ggtaagtt
108       P   V   F   L   S   G   L   E   C   Y

        gtagccta... intron 5 = 1.35kb ...ggctacccattcc

        agAG ACT TCG GAC CTG ACC TGG GAA GAT GAC GAG GAA
118       E   T   S   D   L   T   W   E   D   D   E   E

        GAG GAG GAA GAG GAG GAG GAA GAG GAT GAA GAT GAG
130       E   E   E   E   E   E   E   E   D   E   D   E

        GAT GCA GAT ATA TCG CTA GAG GAG ATA CCT GTC AAA
142       D   A   D   I   S   L   E   E   I   P   V   K

        CAA GTC AAA AGG GTG GCT CCC CAG AAG CAG ATG AGC
154       Q   V   K   R   V   A   P   Q   K   Q   M   S

        ATA GCA AAGgtgggggaaaagaa... intron 6 = 186bp
166       I   A   K

        ...tggtttttgttccagAAA AAG AAG GTG GAA AAA GAA
169                   K   K   K   V   E   K   E

        GAG GAT GAA ACA GTA GTG AGgtaattcatgcagtt...
176       E   D   E   T   V   V   R

        intron 7 = 0.5kb ... ctattccctttccagG CCC AGC
183                                       P   S

        CCT CAG GAC AAG AGT CCC TGG AAG AAG gtgagcaataag
185       P   Q   D   K   S   P   W   K   K

        aag... intron 8 = 92bp ...ctcttatctgcacagGAG
194                                       E

        AAA TCT ACA CCC AGA GCA AAG AAG CCA GTG ACC AAG
195       K   S   T   P   R   A   K   K   P   V   T   K

        AAA TGA CCTCATCTTAGCATCTTCTGCGTCCAAGGCAGGATGTCCA
207       K   *

        GCAGCTGTGTTCTGGTGCAGGTGTCCAGCCCCACCACCCTAGTCTGAA
        TGTAATAAGGTGGTGTGGCTGTAACCCTGTAACCCAGCCCTCCAGTTT
        CCGGAGGTTTTTGGTGAAGAGCCCCCAGCAAGTTCGCCTAGGGCCACA
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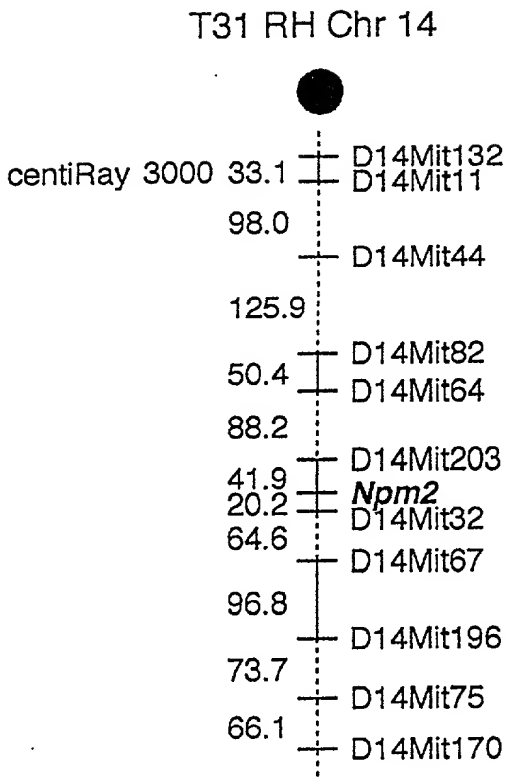
Figure 13B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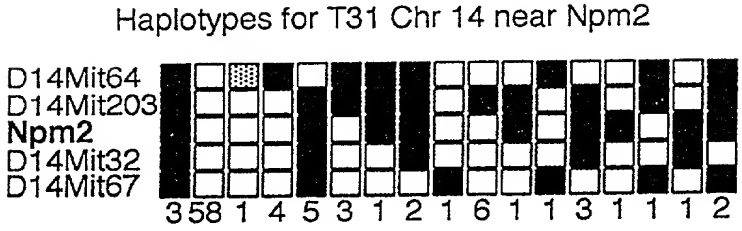
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Figure 14